EXHIBIT A

MPI93-006CP1DV1ACN1DV1M

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10/643,627	Group No.:	1636
August 19, 2003	Examiner:	Guzo, David
RECOMBINANT C140 RECEPTOR ITS AGONISTS AND ANTAGONISTS, AND NUCLEIC ACIDS ENCODING THE RECEPTOR		

Alignment of polypeptide sequences of SEQ ID 4 and SEQ ID 63
SEQ ID 4   398 aa vs. SEQ ID 63   397 aa

ALIGN calculates a global alignment of two sequences
version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
scoring matrix: BLOSUM50, gap penalties: -12/-2
91.8% identity;   Global alignment score: 2342

```
                10        20        30           40        50
/tmp/s  MNVLSFEQTSVTAETPISVMTLVFLSCTGT----NRSSKGRSLIGKVDGTSHVTGKGVTV
        :       .. :...    ...   . :::.::   ::::::::::::::::::::::::::
SEQ     M------RSPSAAWLLGAAILLAASLSCSGTIQGTNRSSKGRSLIGKVDGTSHVTGKGVTV
                10        20        30        40        50

                60        70        80        90       100       110
/tmp/s  ETVFSVDEFSASVLTGKLTTVFLPIVYTIVFVVGLPSNGMALWVFLFRTKKKHPAVIYMA
        :::::::::::::.::::::::::::::::::.:::::::::::::::::::::::::::::
SEQ     ETVFSVDEFSASVLAGKLTTVFLPIVYTIVFAVGLPSNGMALWVFLFRTKKKHPAVIYMA
                60        70        80        90       100       110

               120       130       140       150       160       170
/tmp/s  NLALADLLSVIWFPLKIAYHIHGNNWIYGEALCNVLIGFFYGNMYCSILFMTCLSVQRYW
        ::::::::::::::::::::::::::::::::::::::::::  :::::::::::::::::::
SEQ     NLALADLLSVIWFPLKIAYHIHGNNWIYGEALCNVLIGFFYRNMYCSILFMTCLSVQRYW
               120       130       140       150       160       170

               180       190       200       210       220       230
/tmp/s  VIVNPMGHSRKKANIAIGISLAIWLLILLVTIPLYVVKQTIFIPALNITTCHDVLPEQLL
        :::::::::::::::::::::::::::::  :::::::::::::::::::::::::::::::::
SEQ     VIVNPMGHSRKKANIAIGISLAIWLLTLLVTIPLYVVKQTIFIPALNITTCHDVLPEQLL
               180       190       200       210       220       230

               240       250       260       270       280       290
/tmp/s  VGDMFNYFLSLAIGVFLFPAFLTASAYVLMIRMLRSSAMDENSEKKRKRAIKLIVTVLAM
        :::::::::::::::::::::::::::::::::::::::::::::::::::::::::.:.:
SEQ     VGDMFNYFLSLAIGVFLFPAFLTASAYVLMIRMLRSSAMDENSEKKRKRAIKLIVTVLGM
               240       250       260       270       280       290

               300       310       320       330       340       350
/tmp/s  YLICFTPSNLLLVVHYFLIKSQGQSHVYALYIVALCLSTLNSCIDPFVYYFVSHDFRDHA
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SEQ     YLICFTPSNLLLVVHYFLIKSQGQSHVYALYIVALCLSTLNSCIDPFVYYFVSHDFRDHA
               300       310       320       330       340       350

               360       370       380       390
/tmp/s  KNALLCRSVRTVKQMQVSLTSKKHSRKSSSYSSSSTTVKTSY
        ::::::::::::::::   ::::::::::::::::::::::::::
SEQ     KNALLCRSVRTVKQMQVPLTSKKHSRKSSSYSSSSTTVKTSY
               360       370       380       390
```